

REMARKS

Status of the Claims

Claims 1-9 and 12 and are currently pending in the application. Claims 1-12 stand rejected. Claims 7 and 12 have been amended as set forth herein. Claims 10 and 11 have been cancelled herein. All amendments and cancellations are made without prejudice or disclaimer. No new matter has been added by way of the present amendments. Specifically, the amendment to claim 7 is supported by the specification at, for instance, page 8, lines 2-8. Claim 12 has been amended to change its dependency from cancelled claim 11 to amended claim 7. Reconsideration is respectfully requested.

Rejections Under 35 U.S.C. § 112, Second Paragraph

Claims 10-12 stand rejected under 35 U.S.C. § 112, second paragraph, for failing to particularly point out and distinctly claim the subject matter which Applicants regard as the invention. (*See*, Office Action of February 9, 2007, at page 2, hereinafter "Office Action"). Claims 10 and 11 are cancelled herein without prejudice or disclaimer, thus obviating the rejection as to these claims. Applicants traverse the rejection as to claim 12 as set forth herein.

The Examiner states that the claims are indefinite for reciting amino acid homology without reciting a sequence identifier to which the homology should be compared.

The Examiner's attention is drawn to recent US legal precedent which holds that a specification need not contain a sequence listing where the specification is directed to sequences that are well known in the art. (*See, Faulkner v. Inglis*, 79 U.S.P.Q.2d 1001, 1008 (Fed. Cir. 2006), stating, "Indeed, the forced recitation of known sequences in patent disclosures would only

add unnecessary bulk to the specification. Accordingly we hold that where, as in this case, accessible literature sources clearly provided, as of the relevant date, genes and their nucleotide sequences (here 'essential genes'), satisfaction of the written description requirement does not require either the recitation or incorporation by reference (where permitted) of such genes and sequences.”).

The presently claimed invention is directed to a process for producing an antibody wherein a nonhuman animal with Fas function defects is immunized with a human antigen which has homology of 90% or more at the amino acid sequence level to a homolog protein of the nonhuman animal to be immunized. Thus, the presently claimed invention is not limited to any specific protein. The Inventors herein have discovered a process by which an antibody may be produced in a mouse against a human protein which has a highly homologous protein in the genome of the mouse producing the antibody. Normally such a process presents difficulties since the mouse immune system may generate antibodies that may bind to its own proteins and be detrimental to the mouse's health. The present Inventors discovered that these types of antibodies may be produced by using MRI/lpr mice. Thus, a protein used to generate antibodies in an MRI/lpr mouse is not limited to any specific protein – it may be any protein that has a highly homologous mouse protein.

Reconsideration and withdrawal of the indefiniteness rejection of claim 12 are respectfully requested.

Rejections Under 35 U.S.C. § 102(b)

Kayagaki et al., EP 0872488

Claims 7-10 stand rejected under 35 U.S.C. § 102(b) as being anticipated by Kayagaki et al., EP 0872488 (hereinafter referred to as "Kayagaki et al."). (See, Office Action, at page 2). Claim 10 has been cancelled herein without prejudice or disclaimer, thus obviating the rejection as to claim 10. Applicants traverse the rejection as to claims 7-9 as set forth herein.

The Examiner states that Kayagaki et al. disclose a method for producing an anti-Fas ligand antibody comprising immunizing an MLP/lpr mouse with Fas function defects with a Fas ligand-expressed protein as an antigen. (*Id.*).

However, amended claim 7 now recites, "A process for producing an antibody comprising immunizing a nonhuman animal with Fas function defects with a human antigen which has homology of 90% or more at the amino acid sequence level to a homolog protein of the nonhuman animal to be immunized." Thus, as amended, Kayagaki et al. fail to disclose each and every element of the presently claimed invention, especially the limitation concerning a homology of 90% or more compared to the antigen and any possible mouse homolog thereof.

"A claim is anticipated only if each and every element as set forth in the claim is found, either expressly or inherently described, in a single prior art reference." (See, *Verdegaal Bros. v. Union Oil Co. of California*, 814 F.2d 628, 631, 2 U.S.P.Q.2d 1051, 1053 (Fed. Cir. 1987)). Since Kayagaki et al. do not disclose all elements of the presently claimed invention, Kayagaki et al. do not anticipate the presently claimed invention.

Dependent claims 8 and 9 are not anticipated as, *inter alia*, depending directly or indirectly from a non-anticipated base claim, claim 7.

Reconsideration and withdrawal of the anticipation rejection of claims 7-9 are respectfully requested.

Paul et al., U.S. Patent No. 6,235,714

Claims 7-12 stand rejected under 35 U.S.C. § 102(b) as being anticipated by Paul et al., U.S. Patent No. 6,235,714 (hereinafter referred to as "Paul et al."). (*See*, Office Action, at page 3). Claims 10 and 11 have been cancelled herein without prejudice or disclaimer, thus obviating the rejection as to claims 10 and 11. Applicants traverse the rejection as to claims 7-9 and 12 as set forth herein.

The Examiner states that Paul et al. disclose immunization of MRL/lpr mice with an antigen such as EGFR, TNF α , and IL-1 β to generate catalytic antibodies. (*Id.*). The Examiner further states that the homology of these proteins between human and mouse is 90% to 94% or higher. (*Id.*).

However, amended claim 7 now recites, "A process for producing an antibody comprising immunizing a nonhuman animal with Fas function defects with a human antigen which has homology of 90% or more at the amino acid sequence level to a homolog protein of the nonhuman animal to be immunized." Thus, as amended, Paul et al. fail to disclose each and every element of the presently claimed invention, especially the limitation concerning a homology of 90% or more compared to the antigen and any possible mouse homolog thereof.

Applicants provide attached hereto as Exhibit A sequence alignment data showing the percentage homology between human and mouse EGFR, TNF α and IL- β . Applicants find that these proteins are 78%, 87% and 78% homologous, respectfully. Thus, all antigens to which

antibodies were generated in Paul et al. are lower than 90% homologous between human and mouse. Therefore, Paul et al. do not disclose all of the limitations of the presently claimed invention and cannot anticipate the presently claimed invention, especially as recited in amended claim 7.

"A claim is anticipated only if each and every element as set forth in the claim is found, either expressly or inherently described, in a single prior art reference." (*See, Verdegaa Bros. v. Union Oil Co. of California*, 814 F.2d 628, 631, 2 U.S.P.Q.2d 1051, 1053 (Fed. Cir. 1987)). Since Kayagaki et al. do not disclose all elements of the presently claimed invention, Kayagaki et al. do not anticipate the presently claimed invention.

Dependent claims 8, 9 and 12 are not anticipated as, *inter alia*, depending directly or indirectly from a non-anticipated base claim, claim 7.

Reconsideration and withdrawal of the anticipation rejection of claims 7-9 and 12 are respectfully requested.

Rejections Under 35 U.S.C. § 103(a)

Kayagaki et al. & Fu et al.

Claims 7 and 10-12 stand rejected under 35 U.S.C. § 103(a) as being unpatentable over Kayagaki et al. in view of Fu et al., *Science* 297:2006-2008, 2002 (hereinafter, "Fu et al."). (*See*, Office Action, at page 3). Claims 10 and 11 have been cancelled herein without prejudice or disclaimer, thus obviating the rejection as to claims 10 and 11. Applicants traverse the rejection as to claims 7-9 and 12 as set forth herein.

The Examiner states that Kayagaki et al. do not disclose or suggest an antigen having high homology of between 90% and 94% between mouse and human. (*Id.*). However, the Examiner states that Fu et al. disclose or suggest that mice deficient in either Fas receptor or Fas ligand do not delete autoreactive B cells. (*Id.*). The Examiner further states that it would have been obvious to one of ordinary skill in the art to substitute the Fu et al. mouse to generate antibodies to highly homologous proteins according to the method of Kayagaki et al. (*Id.* at page 4).

Applicants will submit a verified English language translation of the priority document PCT/JP02/08998 following this reply. Thus, the effective filing date of the presently claimed invention of September 4, 2002 will predate the publication date of Fu et al. (September 20, 2002). Thus, Fu et al. will not be available as prior art.

Thus, as admitted by the Examiner, Kayagaki et al. do not disclose or suggest all of the limitations of the presently claimed invention. Therefore, the Examiner has failed to establish a *prima facie* case of obviousness with respect to at least amended claim 7.

Since no specific reasoning is provided for the rejection of dependent claim 12, claim 12 is also believed to be non-obvious for, *inter alia*, depending from a non-obvious base claim, amended claim 7.

Reconsideration and withdrawal of the obviousness rejection of claims 7 and 12 are respectfully requested.

Kayagaki et al., Fu et al. & Veugelers et al.

Claims 1-5 stand rejected under 35 U.S.C. § 103(a) as being unpatentable over Kayagaki et al. in view of Fu et al., and further in view of Veugelers et al., *J. Biol. Chem.*, 274(38):26968-26977, 1999 (hereinafter, "Veugelers et al."). (See, Office Action, at page 4). Applicants traverse the rejection as set forth herein.

The Examiner states that neither Kayagaki et al. nor Fu et al. disclose or suggest the use of glypican protein as an antigen. (*Id.*). However the Examiner finds this limitation in Veugelers et al. which discloses or suggests that glypican-6 has 96% identity between mouse and human and that it would have been obvious to one of ordinary skill in the art to combine the disclosures of all three references to produce antibodies of glypican protein using Applicants' claimed methods.

However, as discussed above, Applicants will submit a verified English language translation of the priority document PCT/JP02/08998. Thus, the effective filing date of the presently claimed invention of September 4, 2002 will predate the publication date of Fu et al. (September 20, 2002).

Thus, as admitted by the Examiner, Kayagaki et al. do not disclose or suggest all of the limitations of the presently claimed invention. Therefore, the Examiner has failed to establish a *prima facie* case of obviousness with respect to independent claims 1 and 2.

Since no specific reasoning is provided for the rejection of dependent claims 3-5, claim 3-5 are also believed to be non-obvious for, *inter alia*, depending from a non-obvious base claim, claims 1 and 2.

Reconsideration and withdrawal of the obviousness rejection of claims 1-5 are respectfully requested.

Kayagaki et al., Fu et al. & Veugelers et al.

Claims 1-56 stand rejected under 35 U.S.C. § 103(a) as being unpatentable over Kayagaki et al. in view of Fu et al., and further in view of Veugelers et al. (*See*, Office Action, at page 4). Applicants traverse the rejection as set forth herein.

As already discussed above, Applicants will submit a verified English language translation of the priority document PCT/JP02/08998 so that the effective filing date of the presently claimed invention will be September 4, 2002, which predates the publication date of Fu et al. (September 20, 2002).

Thus, as admitted by the Examiner, Kayagaki et al. do not disclose or suggest all of the limitations of the presently claimed invention. Therefore, the Examiner has failed to establish a *prima facie* case of obviousness with respect to independent claims 1 and 2.

Since no specific reasoning is provided for the rejection of dependent claims 3-6, claim 3-6 are also believed to be non-obvious for, *inter alia*, depending from a non-obvious base claim, claims 1 and 2.

Reconsideration and withdrawal of the obviousness rejection of claims 1-6 are respectfully requested.

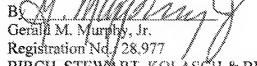
CONCLUSION

If the Examiner has any questions or comments, please contact Thomas J. Siepmann, Ph.D., Registration No 57,374, at the offices of Birch, Stewart, Kolasch & Birch, LLP.

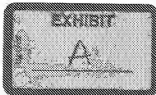
If necessary, the Commissioner is hereby authorized in this, concurrent, and future replies, to charge payment or credit any overpayment to our Deposit Account No. 02-2448 for any additional fees required under 37 C.F.R. § 1.16 or under § 1.17; particularly, extension of time fees.

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Respectfully submitted,


B
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Attachments: Exhibit A – sequence alignments of mouse and human EGFR, TNF α and IL-1 β



Sequences producing significant alignments:

Score
(Bits) E
Value

ref NP_005219.2	epidermal growth factor receptor isoform a [Homo sapiens]	1286	0.0
ref NP_958441.1	epidermal growth factor receptor isoform d [Homo sapiens]	1124	0.0
ref NP_958439.1	epidermal growth factor receptor isoform b [Homo sapiens]	1122	0.0
ref NP_958440.1	epidermal growth factor receptor isoform c [Homo sapiens]	714	0.0
ref NP_001036064.1	v-erb-a erythroblastic leukemia viral oncogene...	705	0.0
ref NP_005226.1	v-erb-a erythroblastic leukemia viral oncogene...	705	0.0
ref NP_001973.2	erbB-3 isoform 1 precursor [Homo sapiens]	639	0.0
ref NP_004439.2	erbB-2 isoform a [Homo sapiens]	624	7e-06
ref NP_001005862.1	erbB-2 isoform b [Homo sapiens]	618	6e-06
ref NP_000499.2	insulin receptor isoform long precursor [Homo sapiens]	119	6e-06
ref NP_001073285.1	insulin receptor isoform short precursor [Homo sapiens]	119	6e-06
ref NP_001005915.1	erbB-3 isoform a precursor [Homo sapiens]	109	1e-06
ref NP_000866.1	insulin-like growth factor 1 receptor precursor [Homo sapiens]	104	2e-06
ref NP_055939.1	insulin receptor-related receptor precursor [Homo sapiens]	95.8	1e-06
ref NP_612199.1	paired basic amino acid cleaving system 4 isoform 1 [Homo sapiens]	52.4	2e-06
ref NP_612194.1	paired basic amino acid cleaving system 4 isoform 2 [Homo sapiens]	52.4	1e-06
ref NP_612192.1	paired basic amino acid cleaving system 4 isoform 3 [Homo sapiens]	51.2	3e-06
ref NP_002561.1	paired basic amino acid cleaving system 4 isoform 4 [Homo sapiens]	51.2	3e-06
ref NP_006131.1	proprotein convertase subtilisin/kexin type 1 [Homo sapiens]	49.3	1e-06
ref NP_025350.1	Fraser syndrome 1 [Homo sapiens]	48.1	3e-06
ref NP_066363.1	zinc finger, NF-kB-type containing 1 [Homo sapiens]	43.5	6e-06
ref NP_060444.1	Swi5 [Homo sapiens]	35.4	0.1
ref NP_006850.1	lipidic acid synthetase isoform 1 precursor [Homo sapiens]	34.7	0.3
ref NP_056295.1	nectin 3 [Homo sapiens]	34.3	0.3
ref NP_019433.1	lipidic acid synthetase isoform 2 precursor [Homo sapiens]	34.3	0.3
ref NP_060042.1	proprotein convertase subtilisin/kexin type 4 [Homo sapiens]	32.3	1.3
ref NP_004186.1	tumor necrosis factor receptor superfamily, member 1 [Homo sapiens]	31.6	2.1
ref NP_062700.1	tumor necrosis factor receptor superfamily, member 2 [Homo sapiens]	31.6	2.1
ref NP_002283.1	laminin, beta 2 precursor [Homo sapiens]	31.6	2.2
ref NP_002323.1	low density lipoprotein-related protein 1 [Homo sapiens]	31.6	2.5
ref NP_004516.1	low density lipoprotein-related protein 2 [Homo sapiens]	31.2	3.1
ref NP_063699.1	tumor necrosis factor receptor superfamily, member 3 [Homo sapiens]	30.8	3.7
ref NP_001035096.1	R-spondin family, member 4 isoform 1 precursor [Homo sapiens]	30.4	5.4
ref NP_000099.1	zinc finger protein 258 [Homo sapiens]	30.4	5.5
ref NP_001025042.1	R-spondin family, member 4 isoform 2 precursor [Homo sapiens]	30.4	5.7
ref NP_055267.1	tumor necrosis factor receptor superfamily, member 4 [Homo sapiens]	30.0	6.1
ref XP_001191279.1	FRS3CD: similar to Fc fragment of IgG [Homo sapiens]	30.0	6.2
ref NP_001699.1	cathopsin B preproprotein [Homo sapiens]	30.0	7.4
ref NP_002550.1	furin preproprotein [Homo sapiens]	29.6	7.6

Alignments

>ref|NP_005219.2| **UG** epidermal growth factor receptor isoform a [Homo sapiens]
Length=1210

Score = 1286 bits (3328), Expect = 0.0, Method: Composition-based stats.
Identities = 627/714 (87%), Positives = 665/714 (93%), Gaps = 2/714 (0%)

Query	1	MRPSTGARTTLLVLLTALCAAGGALKEKKVCGQSTSNRLTQLGTDFHFLSLQRMYNCEV	60
Subject	1	MRPSTGTA LL LL ALA A ALEKKVCGQSTSN+LTLGTDFHFLSLQRMYNCEV	60
Query	61	VLGNLEITTVQRYNDLSFLKTIQEVAGVVLIALNVERIFLENQLIIRGNALYENTYALA	120
Subject	61	VLGNLEITTVQRYNDLSFLKTIQEVAGVVLIALNVERIFLENQLIIRGNALYENTYALA	120
Query	121	YLSNGTNRATGRLRPLMRNLQELLIGAVRFSNNPILCNHDDITQWRDIVQNVFNSNMHDL	180
Subject	121	+LSNY N+TGL+ELPMKRLQELLIGAVRFSNNPILCNHDDITQWRDIVQNVFNSNMHDL	180
Query	181	QSHPSGCCPKLHPCSPNGSCWGGGEENCQKLTIIICAQGCSSHRGRSPSDCCNQCACGC	240
Subject	181	QNLGSCQKCDPSCPNNGSCWGGGEENCQKLTIIICAQGCSSHRGRSPSDCCNQCACGC	240
Query	241	TGPRSDCLVCGKPDDEATCKDTCFPLMLNPTTYQMDVNPBGKYSFGATCVKKCPRNVY	300
Subject	241	TGPRSDCLVCGKPDDEATCKDTCFPLMLNPTTYQMDVNPBGKYSFGATCVKKCPRNVY	300
Query	301	VTDHGSCVRACGPDYEVVEEDGIRKCKKCDGFCRKCVCNGIGIGFCKDTLSINATNIRHKF	360
Subject	301	VTDHGSCVRACGPDYEVVEEDGIRKCKKCDGFCRKCVCNGIGIGFCKDTLSINATNIRHKF	360
Query	361	YCTALSGDHLITPVATGDSFTHTPLDPRLEILKTVKEITGFLIQWPDHWDHDLHAF	420
Subject	361	CT+YSGDHLITPVATGDSFTHTPLDPRLEILKTVKEITGFLIQWPDHWDHDLHAF	420
Query	421	ENLEIIRGTRQHGQSLAVVGLNITSLGLRLSKLSESDGVLSIENRNLCYANTINWKKL	480
Subject	421	ENLEIIRGTRQHGQSLAVVGLNITSLGLRLSKLSESDGVLSIENRNLCYANTINWKKL	480
Query	481	FGTNPQTKTKHNNRAKCKKAVNHCNPLCSSGCGPEPRDCVSCONVSRGREGCVKKN	540
Subject	481	FGTNPQTKTKHNNRAKCKKAVNHCNPLCSSGCGPEPRDCVSCONVSRGREGCVKKN	540
Query	541	ILGSGPREFVENSECTQCHPFLQAMNITTCGRGPDNCTQCAHIDSGFVCKTCFAGIM	600
Subject	541	ILGSGPREFVENSECTQCHPFLQAMNITTCGRGPDNCTQCAHIDSGFVCKTCFAGIM	600
Query	601	GENNTLVNKLADANNVCHLCHANCITYGCAQGLGCGEVHTSGKIPSTANGTVGLGLIV	660
Subject	601	GENNTLVNKLADANNVCHLCHANCITYGCAQGLGCGEVHTSGKIPSTANGTVGLGLIV	660
Query	661	VVALGIGLEMMRRNHHVKKRTRLRLQRELVEPLTSPSEAPNQHRLRLKETEF	714
Subject	659	VVALGIGLEMMRRNHHVKKRTRLRLQRELVEPLTSPSEAPNQHRLRLKETEF	712

>res|NP_95441.1| **UG** epidermal growth factor receptor isoform d [Homo sapiens]
Length=705

Score = 1124 bits (2907), Expect = 0.0, Method: Composition-based stats.
Identities = 554/635 (87%), Positives = 588/635 (92%), Gaps = 0/635 (0%)

Query	1	MRPSTGARTTLLVLLTALCAAGGALKEKKVCGQSTSNRLTQLGTDFHFLSLQRMYNCEV	60
Subject	1	MRPSTGTA LL LL ALA A ALEKKVCGQSTSN+LTLGTDFHFLSLQRMYNCEV	60
Query	61	VLGNLEITTVQRYNDLSFLKTIQEVAGVVLIALNVERIFLENQLIIRGNALYENTYALA	120
Subject	61	VLGNLEITTVQRYNDLSFLKTIQEVAGVVLIALNVERIFLENQLIIRGNALYENTYALA	120
Query	121	YLSNGTNRATGRLRPLMRNLQELLIGAVRFSNNPILCNHDDITQWRDIVQNVFNSNMHDL	180
Subject	121	+LSNY N+TGL+ELPMKRLQELLIGAVRFSNNPILCNHDDITQWRDIVQNVFNSNMHDL	180
Query	181	QSHPSGCCPKLHPCSPNGSCWGGGEENCQKLTIIICAQGCSSHRGRSPSDCCNQCACGC	240
Subject	181	QNLGSCQKCDPSCPNNGSCWGGGEENCQKLTIIICAQGCSSHRGRSPSDCCNQCACGC	240
Query	241	TGPRSDCLVCGKPDDEATCKDTCFPLMLNPTTYQMDVNPBGKYSFGATCVKKCPRNVY	300
Subject	241	TGPRSDCLVCGKPDDEATCKDTCFPLMLNPTTYQMDVNPBGKYSFGATCVKKCPRNVY	300
Query	301	VTDHGSCVRACGPDYEVVEEDGIRKCKKCDGFCRKCVCNGIGIGFCKDTLSINATNIRHKF	360

Sequences producing significant alignments:		Score (bits)	E Value
ref NP_000585.2	tumor necrosis factor alpha [Homo sapiens]	372	1e-
ref NP_000585.2	lymphotoxin alpha precursor [Homo sapiens]	85.5	4e-
ref NP_005109.2	tumor necrosis factor (ligand) superfamily, ...	74.3	7e-
ref NP_003798.2	tumor necrosis factor ligand superfamily, me...	66.2	2e-
ref NP_742011.1	tumor necrosis factor ligand superfamily, me...	66.2	2e-
ref NP_000630.1	Tas ligand [Homo sapiens]	57.4	9e-
ref NP_002332.1	lymphotoxin-beta isoform a [Homo sapiens]	56.2	2e-
ref NP_002692.1	tumor necrosis factor ligand superfamily, me...	52.0	4e-
ref NP_143026.1	tumor necrosis factor ligand superfamily, me...	52.0	4e-
ref NP_003801.1	tumor necrosis factor (ligand) superfamily, ...	43.5	2e-
ref NP_000955.1	CD40 ligand [Homo sapiens]	38.5	0.0
ref NP_742086.1	tumor necrosis factor (ligand) superfamily, ...	32.0	0.4
ref NP_003799.1	tumor necrosis factor ligand superfamily, me...	31.2	0.6
ref NP_742084.1	tumor necrosis factor ligand superfamily, me...	31.2	0.6
ref NP_742085.1	tumor necrosis factor ligand superfamily, me...	31.2	0.6
ref NP_005564.1	tumor necrosis factor (ligand) superfamily, ...	31.2	0.6
ref NP_001235.1	tumor necrosis factor (ligand) superfamily, ...	29.3	2.9
ref NP_001003399.1	bicaudal D homolog 1 isoform 2 [Homo sapiens]	27.7	7.2
ref NP_001705.2	bicaudal D homolog 1 isoform 1 [Homo sapiens]	27.7	8.0
ref NP_054835.2	hypothetical protein LOC29035 [Homo sapiens]	27.3	9.3

Alignments

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>ref|NP_000585.2| UG tumor necrosis factor alpha [Homo sapiens]
Length=233

Score = 372 bits (956), Expect = 1e-103, Method: Composition-based stats.
Identities = 186/236 (78%), Positives = 211/236 (89%), Gaps = 4/236 (1%)

Query 1 MSTEEMIRDELALAEALPQKMGCPQNSRRCLCLSLFSLFVAGATTLPCLLNFGSVIGPQR 60
Sbjct 1 MSTEEMIRDELALAEALP+K GG Q SRRL LSLPSEF+VAGATTLPCLLNFGSVIGPQR
MSTEEMIRDELALAEALPKRTGGPQSGRRCLFLSLFSLFVAGATTLPCLLNFGSVIGPQR 60

Query 61 DEKTFNGPLISSMAQTTLRGSQ--NSSEKPFVAVVAVNHQVEEQLEWLSQRALLANGM 120
+L+DNLVVP++GLYL+YSVLFKGGCP +VLLTH+SR A+SYQ KVNLLA+KSPC
EE-TPRDLSELISLAQAV--RSESRTPSKPFVAVVAVNPQAEQQLQWLNRRALLANGV 117

Query 121 DLKNDNLVVPADGLYLVSQVLFKGGCPD-VVLLTH+VSRFAISYQEKVNLLSAVKSPC 179
+L+DNLVVP++GLYL+YSVLFKGGCP +VLLTH+SR A+SYQ KVNLLA+KSPC
ELRWDLVVPSEGLYLVSQVLFKGGCPSTVLLTH+VSRFAISYQEKVNLLSAVKSPC 177

Query 180 PKDPFEGAEALPWFYFPIYLGAVPTLRSDQLSAEKNVLPKLLPFAESQGVVFGIAL 235
++TPECAE KPWYKPIYLGAVPTLRSDQLSAEKNVLPKLLPFAESQGVVFGIAL
Sbjct 176 QRTPEGAELPWFYFPIYLGAVPTLRSDQLSAEKNVLPKLLPFAESQGVVFGIAL 233

>ref|NP_000586.2| UG lymphotoxin alpha precursor [Homo sapiens]
Length=205

Score = 85.5 bits (210), Expect = 4e-17, Method: Composition-based stats.
Identities = 61/176 (34%), Positives = 86/176 (48%), Gaps = 14/176 (7%)

Query 67 GLPLSSMAQTTLRGSQ--NSSEKPFVAVVAVNHQVEEQLEWLSQRALLANGMDLK 124
+L+L S AQH +S+ KP AH++ + +LW+ A L+G LK
Sbjct 37 GVGLTSAATQARQPKMHLANSTLPAANHLGDSKQNSLWRNNTDRAFLQGFSLN 96

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Sequences producing significant alignments:		Score (Bits)	E Value
ref NP_000567.1 	interleukin 1, beta proprotein [Homo sapiens]	232	9e-
ref NP_775270.1 	interleukin 1 family, member 8 isoform 2 [Homo	59.7	7e-
ref NP_776214.1 	interleukin 1 receptor antagonist isoform 1 ...	58.9	2e-
ref NP_000568.1 	interleukin 1 receptor antagonist isoform 3 [Ho	58.2	3e-
ref NP_776215.1 	interleukin 1 receptor antagonist isoform 4 [Ho	58.2	3e-
ref NP_776219.1 	interleukin 1 receptor antagonist isoform 2 [Ho	58.2	3e-
ref NP_115345.1 	interleukin 1 family, member 10 [Homo sapiens]...	51.6	2e-
ref NP_035407.1 	interleukin 1 family, member 5 [Homo sapiens]...	47.8	4e-
ref NP_062564.1 	interleukin 1 family, member 9 [Homo sapiens]	40.8	4e-
ref NP_775295.1 	interleukin 1 family, member 7 isoform 3 [Homo	36.6	0.0
ref NP_775296.1 	interleukin 1 family, member 7 isoform 4 [Homo	36.6	0.0
ref NP_775294.1 	interleukin 1 family, member 7 isoform 2 [Homo	36.2	0.0
ref NP_775297.1 	interleukin 1 family, member 7 isoform 5 [Homo	36.2	0.0
ref NP_055254.2 	interleukin 1 family, member 7 isoform 1 pro...	35.8	0.0
ref NP_055255.1 	interleukin 1 family, member 6 (epsilon) [Homo	35.6	0.0
ref NP_055253.2 	interleukin 1 family, member 8 isoform 1 [Homo	32.0	0.1
ref NP_000566.1 	interleukin 1, alpha proprotein [Homo sapiens]	29.6	0.8
ref NP_036243.1 	AKAP, activator of heat shock 90kDa protein ...	29.6	0.9
ref NP_000565.1 	cell-1 suppressor of lin-12-like [Homo sapiens]	28.9	1.6
ref NP_000227.1 	lipase C precursor [Homo sapiens]	28.5	2.1
ref NP_000492.1 	thyroid hormone receptor, beta [Homo sapiens]	27.3	4.7
ref NP_000606.1 	neural cell adhesion molecule 1 isoform 1 [Homo	26.6	8.1
ref NP_051096.2 	neural cell adhesion molecule 1 isoform 2 [Homo	26.6	8.9

Alignments

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>ref|NP_000567.1| UG interleukin 1, beta proprotein [Homo sapiens]
Length=269

Score = 232 bits (591), Expect = 3e-62, Method: Composition-based stats.
Identities = 119/152 (78%), Positives = 132/152 (86%), Gaps = 1/152 (0%)

Query 2  PIRQHYRLADSDQKSLVLSDFYELKALHLNCGMINCOVIFSMFVQGEPSNDKIPVALG 51
      P+R L+ LRD QKSLV+S FYELKALHL GQ++ QGV+FSMSFVQGE SNDKIPVALG
Sbjct 118  PVRSLNGLRLDSDQKSLVLSDFYELKALHLGQGGDMQGVVFSMSFVQGEESNDKIPVALG 177

Query 62  LKGNKLYLSCVMKDGPTTLOLESVDPKQYPKCKMEKRFVFNKIEVKSKEVFESAEFPNNWY 121
      LR NMLSCV+RD PTLQLESVDPK YPKCKMEKRFVFNKIE+ +K+EFESA+FPNNWY
Sbjct 178  LKEKNLILSCVLRDDEKPTLQLESVDPKYPKCKMEKRFVFNKIEENKLESFESAEFPNNWY 237

Query 122  ISTSQAEKHPVFL-GNNSGQOILDFIMKSVSS 152
      ISTSQAE+ PVFL G GDI DFIM+ VSS
Sbjct 238  ISTSQARNHPVFLGGTKGGQDITDFIMQFVSS 269

>ref|NP_775270.1| UG interleukin 1 family, member 8 isoform 2 [Homo sapiens]
Length=157

Score = 59.7 bits (143), Expect = 7e-10, Method: Composition-based stats.
Identities = 36/95 (37%), Positives = 54/95 (56%), Gaps = 2/95 (2%)

Query 58  VALGLKGNLHLSCVMKDGPTTLOLESVDPKQYPKCKMEKRFVFNKIEVKSKEVFESAE 116
      VLG+RGK+L L C G PTLQL+ + Y +K +K P+P+
Sbjct 62  VYLGIKGNLHLSCVLRDDEKPTLQLESVDPKYPKCKMEKRFVFNKIEENKLESFESAE 121

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